

LOCUS TOMWIP1 660 bp mRNA linear PIN 27-APR-1993
 DEFINITION Tomato leaf wound-induced proteinase inhibitor II mRNA, complete cds.
 ACCESSION K03291
 VERSION K03291.1 GI:170521
 KEYWORDS protease inhibitor; wound-induced protease inhibitor.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 Graham, J.S., Pearce, G., Merryweather, J., Tilt, K., Ericson, L.H. and Ryan, C.A.
 Wound-induced proteinase inhibitors from tomato leaves. II. The CDNA-decoded primary structure of pre-inhibitor II
 J. Biol. Chem. 260 (11), 6561-6564 (1985)
 MEDLINE 85207658
 PUBMED 3838986
 COMMENT Original source text: Tomato (L. esculentum L. var. Bonnie Best) wounded leaf, CDNA to mRNA, clone pri-24.
 A 10 bp palindrome identical to the one following the TOMWIP1 cds (see separate entry) begins at position 566 [1]. A polyadenylation signal is present at position 638-643 [1].
 A printed copy of this sequence was kindly provided by C.A. Ryan (18-SEP-1985).

FEATURES
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 124..492
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 279 bp upstream of Sau3A site.

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 ATGTGATGCCAAGGCTTGACTAGAGATGTGT 109
 |||
 113 ATGTGATGCCAAGGCTTGACTAGAGATGTGT 147

RESULT 5
 LOCUS AY007240 684 bp DNA linear PIN 02-JAN-2001
 DEFINITION Lycopersicon esculentum proteinase inhibitor II gene, complete cds.
 ACCESSION AY007240
 VERSION AY007240.1 GI:12007535
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 Xie, X. and Wu, N.
 Isolation of tomato proteinase inhibitor II gene and analysis of

JOURNAL its structure
 REFERENCE 2 Unpublished
 AUTHORS Xie, X. and Wu, N.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-2000) Plant Developmental Molecular Biology,
 Institute of Developmental Biology, Chinese Academy of Sciences,
 Nanjing No. 3, Zhongguancun, Haidian District, Beijing 100080,
 China

FEATURES
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ORIGIN
 Query Match 6.6%; Score 35; DB 8; Length 684;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 ATGTGATGCCAAGGCTTGACTAGAGATGTGT 109
 |||
 182 ATGTGATGCCAAGGCTTGACTAGAGATGTGT 216

RESULT 6
 LOCUS AY422686 687 bp mRNA linear PIN 18-MAY-2004
 DEFINITION Solanum nigrum proteinase inhibitor 2b precursor (PIN2b) mRNA,
 complete cds.
 ACCESSION AY422686
 VERSION AY422686.1 GI:40036963
 KEYWORDS
 SOURCE Solanum nigrum (black nightshade)
 ORGANISM Solanum nigrum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
 Schmidt, D.D., Kessler, A., Kessler, D., Schmidt, S., Lim, M., Gase, K. and Baldwin, I.T.
 Solanum nigrum: a model ecological expression system and its tools
 Mol. Ecol. 13 (5), 981-995 (2004)
 2 (bases 1 to 687)
 Schmidt, D.D., Gase, K. and Baldwin, I.T.
 Direct Submission
 Submitted (25-SEP-2003) Molecular Ecology, Max Planck Institute for
 Chemical Ecology, Hans-Knoell-Strasse 8, Jena D-07745, Germany

FEATURES
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 00:50:47 ; Search time 3110 Seconds
(without alignments)
6474.598 Million cell updates/sec

Title: US-10-725-829-1

Perfect score: 529

Sequence: 1 cataatgctgcgttcacaaag.....ctgtaatgctgacttattcg 529

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	6.6	313	4	BG628044 CC-estf1cL
2	35	6.6	331	4	BG628003 CC-estf1cL
3	35	6.6	370	2	AM092618 EST285798
4	35	6.6	379	1	A1486303 EST244624
5	35	6.6	401	2	BE463220 EST354443
6	35	6.6	420	1	A1899171 EST268614
7	35	6.6	421	1	A1488891 EST247230
8	35	6.6	424	1	A1483908 EST249779
9	35	6.6	447	1	A1488484 EST246823
10	35	6.6	469	1	A1489746 EST248085
11	35	6.6	469	2	AM929301 EST338089
12	35	6.6	476	2	AM041477 EST284341
13	35	6.6	476	2	AM091675 EST284771
14	35	6.6	477	2	AM093009 EST286189
15	35	6.6	484	2	BE463283 EST354506
16	35	6.6	487	2	AM217702 EST252646
17	35	6.6	501	1	A1771251 EST252267
18	35	6.6	503	2	AM221025 EST297494
19	35	6.6	504	1	A1485972 EST244293
20	35	6.6	515	1	A1489819 EST248158
21	35	6.6	533	1	A1771306 EST252322
22	35	6.6	534	4	B1932530 EST552419
23	35	6.6	541	2	AM929269 EST338057
24	35	6.6	550	1	A1485979 EST244300

25	35	6.6	558	2	AM092640 EST285820
26	35	6.6	564	2	BE354745 EST354835
27	35	6.6	567	2	AM217791 EST296505
28	35	6.6	571	1	A1771944 EST253044
29	35	6.6	580	4	B1930517 EST350406
30	35	6.6	581	4	B1929125 EST549014
31	35	6.6	582	1	BE354912 EST355002
32	35	6.6	587	1	A1484805 EST243066
33	35	6.6	593	4	B1935978 EST555867
34	35	6.6	604	1	A1487479 EST245801
35	35	6.6	623	4	B1930668 EST550557
36	35	6.6	623	4	B1930919 EST550808
37	35	6.6	623	4	B1932864 EST552753
38	35	6.6	624	2	AM093425 EST286605
39	35	6.6	626	4	B1929471 EST549360
40	35	6.6	629	2	AM217790 EST296504
41	35	6.6	630	4	B1931013 EST550902
42	35	6.6	637	2	BE463161 EST354300
43	35	6.6	644	4	B1935830 EST555719
44	35	6.6	645	4	BG125289 EST470935
45	35	6.6	647	2	BE463390 EST354613

ALIGNMENTS

RESULT 1
LOCUS BG628044 313 bp mRNA linear EST 19-APR-2001
DEFINITION CC-estf1cL:LN23b1 Tomato flower library from a mixture of developmental stages Lycopersicon esculentum cDNA clone.
CC-estf1cL:LN23b1. mRNA sequence.

ACCESSION BG628044
VERSION BG628044.1 GI:13679517
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum

REFERENCE
AUTHORS van der Hoeven, R.S. and Tanksley, S.D.
TITLE ESTs from a tomato flower library.
JOURNAL Unpublished (2001)
COMMENT Contact: Rutgers S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv13@cornell.edu

FEATURES

source
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/dev_stage="4-8 week old plants"
/lab_host="XIOIR"
/clone_lib="Tomato flower library from a mixture of developmental stages"
/note="Vector: pBK CMV; Site_1: EcoRI; Site_2: XhoI; flowers and flower buds were collected from greenhouse grown plants and used for library construction (cLEL)."

ORIGIN

Query Match 6.6%; Score 35; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 109

Db	90	ATGTTGATGCCAAGCGCTTGTAAGATGATGCT 124
RESULT 2	BG629003	331 bp mRNA linear EST 19-APR-2001
LOCUS	cc-ef5fclEL24013d1	Tomato flower library from a mixture of developmental stages
DEFINITION	cc-ef5fclEL24013d1	Lycopersicon esculentum cDNA clone
ACCESSION	BG629003	
VERSION	BG629003.1	GI:13680476
KEYWORDS	EST.	
SOURCE	Lycopersicon esculentum (tomato)	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.	
REFERENCE	1 (bases 1 to 331)	
AUTHORS	van der Hoeven, R.S. and Tanksley, S.D.	
TITLE	ESTs from a tomato flower library	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Rutgers S. van der Hoeven Cornell University 252 Emerson Hall, Ithaca, NY 14850, USA Tel: 607 255 7886 Fax: 607 255 6683 Email: rv19@cornell.edu 3 prime sequence.	
FEATURES	Location/Qualifiers	
Source	1..331	
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	/dev_stage="4-8 week old plants"	
	/lab_host="XLOLR"	
	/clone_lib="Tomato flower library from a mixture of developmental stages"	
	/note="Vector: pBK CMV; Site 1: EcoRI; Site 2: XhoI; flowers and flower buds were collected from greenhouse grown plants and used for library construction (cLEL)."	
ORIGIN		
Query Match	6.6%; Score 35; DB 4; Length 331;	
Best Local Similarity	100.0%; Pred. No. 3.2e-07;	
Matches	35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Y	75 ATGTTGATGCCAAGCGCTTGTAAGATGATGCT 109	
Db	265 ATGTTGATGCCAAGCGCTTGTAAGATGATGCT 299	
RESULT 3	AM092618	370 bp mRNA linear EST 18-MAY-2001
LOCUS	EST285798	tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLEF21C15, mRNA sequence.
ACCESSION	AM092618	
VERSION	AM092618.1	GI:6058213
KEYWORDS	EST.	
SOURCE	Lycopersicon esculentum (tomato)	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.	
REFERENCE	1 (bases 1 to 370)	
AUTHORS	D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.	

```

TITLE      Generation of ESTs from tomato leaf tissue
JOURNAL    Unpublished (1999)
COMMENT     Clemson University Genomics Institute
            Contact: CUGI
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
FEATURES   location/Qualifiers
SOURCE     1..370
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            /lab_host="XLI-Blue MRP"
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            /clone_1b="Tomato mixed elicitor, BRT"
            /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; CLEF - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisocoumaric acid, BTH, jasmonic acid, ethylene, fenchone, Eix, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
ORIGIN
Query Match          6.6%; Score 35; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dn                    31 ATGTTGATGCCAAGCGCTTGACTACGAGAATGTGGT 65
Oy                    75 ATGTTGATGCCAAGCGCTTGACTACGAGAATGTGGT 109
                        |||||
                        |||||
                        |||||
LOCUS           AI1486303               379 bp      mRNA       linear   EST 18-MAY-2001
DEFINITION      EST244624 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
KEYWORDS         CLED8M22, mRNA sequence.
ACCESSION        AI1486303
VERSION          AI1486303.1 GI:4381674
SOURCE           EST.
ORGANISM         Lycopersicon esculentum (tomato)
                Lycopersicon esculentum
                Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE        1 (bases 1 to 379)
AUTHORS          Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
                  Holt,I.E., Liang,F., Upton,J., Romning,C.M., Craven,M.B.,
                  Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C.,
                  Martin,G.B., Tanksey,S.D. and Giovannoni J.
                  Generation of ESTs from tomato carpel tissue
                  Unpublished (1999)
COMMENT          Contact: CUGI
                  Clemson University Genomics Institute
                  Clemson University
                  100 Jordan Hall, Clemson, SC 29634, USA
                  Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES         Location/Qualifiers
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ORIGIN

XhoI, cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

Query Match 6.6%; Score 35; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGT 109
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59 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGT 133

RESULT 5
BE463220 401 bp mRNA linear EST 18-MAY-2001
LOCUS BE463220

DEFINITION EST154443 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone cT0C12K7, mRNA sequence.

ACCESSION BE463220
VERSION BE463220.2 GI:11387851
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 401)

REFERENCE
AUTHORS Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Romling, C.M., Fraser, C.M., Martin, G.B., Giovannoni, J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue
Unpublished (1999)
On Jul 27, 2000 this sequence version replaced gi:9508991.
Contact: CUGI

TITLE
JOURNAL
COMMENT
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source location/Qualifiers

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/clone_lib="tomato flower buds 8 mm to pre-anthesis, Cornell University"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGT 109
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RESULT 6
A1899171 420 bp mRNA linear EST 18-MAY-2001
LOCUS A1899171

DEFINITION EST268614 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED37020, mRNA sequence.

ACCESSION A1899171
VERSION A1899171.1 GI:5650573-
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 420)

REFERENCE
AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Romling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Niernan, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI

TITLE
JOURNAL
COMMENT
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source location/Qualifiers
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match 6.6%; Score 35; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGT 109
|||||
92 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGT 126

RESULT 7
A1488891 421 bp mRNA linear EST 18-MAY-2001
LOCUS A1488891
DEFINITION EST247230 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED31119, mRNA sequence.

ACCESSION A1488891
VERSION A1488891.1 GI:4384262
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 421)

REFERENCE
AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Romling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Niernan, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
Location/Qualifiers

FEATURES

SOURCE

1. 421
/organism="Lycopersicon esculentum"
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/lab_host="XLI-Blue MRP"
/clone_lib="tomato ovary, TAMU"
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ORIGIN

Query Match

Best Local Similarity 6.6%; Score 35; DB 1; Length 421;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 109
111 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 145

Db

RESULT 8
LOCUS A1483908 424 bp mRNA linear EST 18-MAY-2001

DEFINITION EST248779 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLEDD24119, mRNA sequence.

ACCESSION A1483908

VERSION A1483908.1 GI:4387832

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE 1 (bases 1 to 424)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)

AUTHORS

Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.

Generation of ESTs from tomato carpel tissue
Unpublished (1999)

CONTACT: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1. 424

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CLEDD24119"

/tissue_type="carpel"

/dev_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab_host="XLI-Blue MRP"

/clone_lib="tomato ovary, TAMU"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match

6.6%; Score 35; DB 1; Length 424;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 109
92 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 126

Db

RESULT 9
LOCUS A1488484 447 bp mRNA linear EST 18-MAY-2001

DEFINITION EST246823 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLEDD3F12, mRNA sequence.

ACCESSION A1488484

VERSION A1488484.2 GI:11388182

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE 1 (bases 1 to 447)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)

AUTHORS

Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)

CONTACT: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

POLYA=No.

Location/Qualifiers

1. 447

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CLEDD3F12"

/tissue_type="carpel"

/dev_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab_host="XLI-Blue MRP"

/clone_lib="tomato ovary, TAMU"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match 6.6%; Score 35; DB 1; Length 447;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 109
98 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGGT 132

Db

RESULT 10
LOCUS A1489746 469 bp mRNA linear EST 18-MAY-2001

DEFINITION EST248085 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLEDD14D15, mRNA sequence.

ACCESSION A1489746

VERSION A1489746.1 GI:4385117

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE 1 (bases 1 to 469)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Niernan,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)

REFERENCE
AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 469)

TITLE
JOURNAL
COMMENT

Alcala, J., Vrebalov, J., White, R., Matern, A. L., Viston, T., Holt, I. E., Liang, F., Upton, J., Ranning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Niernan, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)

FEATURES

Source

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
Location/Qualifiers
1..469

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 35; DB 1; Length 469;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

75 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 109
|||||
111 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 145

RESULT 11
AM929301
LOCUS

AW929301 469 bp mRNA linear EST 18-MAY-2001
EST338089 tomato flower buds 8 mm to pre-anthesis, Cornell
University Lycopersicon esculentum cDNA clone CT0C7019 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS

AW929301
AW929301.1 GI:8104702
EST.

SOURCE
ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum

REFERENCE
AUTHORS

van der Hoeven, R. S., Bezzerides, J. L., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Ranning, C. M., Fraser, C. M., Martin, G. B., Giovannoni, J. J. and Tanksley, S. D.
Generation of ESTs from tomato flower tissue
Unpublished (1999)

TITLE
JOURNAL
COMMENT

Clemson University Genomics Institute
Contact: CUGI

FEATURES

Source

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
5 prime sequence.
Location/Qualifiers
1..469
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultiyar="TA496"

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

75 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 109
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78 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 112

RESULT 12
AM041477
LOCUS

AM041477 476 bp mRNA linear EST 18-MAY-2001
EST284341 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA
clone CLE114H6, mRNA sequence.

ACCESSION
VERSION
KEYWORDS

AM041477
AM041477.1 GI:5900231
EST.

SOURCE

Lycopersicon esculentum (tomato)
Lycopersicon esculentum

REFERENCE
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 476)
D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Liang, F., Upton, J., Ranning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Niernan, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)

TITLE
JOURNAL
COMMENT

Clemson University Genomics Institute
Contact: CUGI

Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
3 prime sequence.
Location/Qualifiers
1..476

FEATURES

Lycopersicon esculentum
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultiyar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="CLE114H6"
/tissue_type="leaf"
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/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLEF - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

75 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 109
|||||

Db 108 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 142

RESULT 13
LOCUS AM091675
DEFINITION EST284771 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA
ACCESSION AM091675
VERSION AM091675.1 GI:6057186
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 476)
D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Liang, F., Upton, J., Roming, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nierman, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..476
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
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/clone="cLET14H6"
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/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 109
|||||
Db 108 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 142

RESULT 14
LOCUS AM093009
DEFINITION AM286189 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA
ACCESSION AM093009
VERSION AM093009.1 GI:6058604
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 477)
D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Liang, F., Upton, J., Roming, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nierman, W.,

Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..477
/organism="Lycopersicon esculentum"
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ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 109
|||||
Db 72 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 106

RESULT 15
LOCUS BE463283
DEFINITION BE334506 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone CTC1206, mRNA sequence.
ACCESSION BE463283
VERSION BE463283.1 GI:9509056
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 484)
van der Hoeven, R. S., Bezzerides, J. L., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Roming, C. M., Fraser, C. M., Martin, G. B., Giovannoni, J. J. and Tanksley, S. D.
Generation of ESTs from tomato flower tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..484
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTC1206"
/tissue_type="flower"

/dev stage="buds 8mm-to-preanthesis"
/clone.lib="tomato flower buds 8 mm to pre-anthesis,
Cornell University"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tankeley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 484;
Best Local Similarity 100.0%; Pred.No.3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGCT 109
|||
Db 98 ATGTTGATGCCAAGGCTTGTTACTAGAGATGTGCT 132

Search completed: August 22, 2005, 04:52:01
Job time : 317 secs

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9	20	2.0	022	20	US-10-723-022-3	Sequence 3, Appli

8	20	3.8	1104	14	US-10-164-961-1	Sequence 1, Appl1
9	20	3.8	1104	17	US-10-157-622-1	Sequence 1, Appl1
10	20	3.8	1104	17	US-10-072-809A-56	Sequence 56, Appl1
11	20	3.8	1104	24	US-11-062-999-56	Sequence 56, Appl1
12	20	3.8	1167	18	US-10-425-114-36251	Sequence 36251, A
13	20	3.8	1360	10	US-09-812-502-2	Sequence 2, Appl1
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16	20	3.8	1417	18	US-10-425-114-28622	Sequence 28622, A
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18	20	3.8	8693	15	US-10-311-455-782	Sequence 782, A
19	19	3.6	360	19	US-10-767-795-1449	Sequence 1449, Appl1
20	19	3.6	406	11	US-09-732-627A-1716	Sequence 1716, Appl1
21	19	3.6	683	13	US-10-027-632-244456	Sequence 244426, A
22	19	3.6	683	17	US-10-027-632-244456	Sequence 244426, A
23	19	3.6	875	19	US-10-767-795-1428	Sequence 1428, Appl1
24	19	3.6	25899	19	US-10-332-666-10	Sequence 10, Appl1
25	19	3.6	394468	21	US-10-741-600-17952	Sequence 17952, A
26	18	3.4	507	13	US-10-027-632-186836	Sequence 186836, A
27	18	3.4	507	17	US-10-027-632-186836	Sequence 186836, A
28	18	3.4	522	13	US-10-027-632-278489	Sequence 278489, A
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30	18	3.4	717	17	US-10-282-122A-22378	Sequence 22378, A
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32	18	3.4	2291	19	US-10-761-169-9	Sequence 9, Appl1
33	18	3.4	2456	11	US-09-939-853A-33	Sequence 34, Appl1
34	18	3.4	2456	11	US-09-939-853A-36	Sequence 36, Appl1
35	18	3.4	2636	17	US-10-104-047-635	Sequence 635, Appl1
36	18	3.4	2803	17	US-10-104-047-1912	Sequence 1912, Appl1
37	18	3.4	2898	10	US-09-764-891-9475	Sequence 9475, A
38	18	3.4	2898	10	US-09-764-891-9476	Sequence 9476, A
39	18	3.4	2898	15	US-10-205-428-856	Sequence 856, Appl1
40	18	3.4	2898	15	US-10-205-428-857	Sequence 857, Appl1
41	18	3.4	2907	17	US-10-037-270-511	Sequence 511, Appl1
42	18	3.4	2907	17	US-10-037-272-511	Sequence 511, Appl1
43	18	3.4	4356	17	US-10-282-122A-27222	Sequence 27222, A
44	18	3.4	4908	17	US-10-282-122A-33044	Sequence 33044, A
45	18	3.4	5092	9	US-09-996-956-3	Sequence 3, Appl1

ALIGNMENTS

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1 RESULT 1
2 US-10-725-829-1
3 ; Sequence 1, Application US/10725829
4 ; Publication No. US20040205846A1
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Chye, Mee Len
9 ; APPLICANT: Xu, Zeng-Fu
10 ;
11 ; TITLE OF INVENTION: Genetically Modified Plants with Heterogenous Proteinase Inhibitor
12 ; TITLE OF INVENTION: Sln, Suk Fong
13 ; TITLE OF INVENTION: SapIN2A or SapIN2B and Methods of Use Thereof for the Inhibition
14 ; TITLE OF INVENTION: of Trypsin- and Chymotrypsin-Like Activities
15 ;
16 ; FILE REFERENCE: 9661-043-989
17 ;
18 ; CURRENT APPLICATION NUMBER: US/10/725,829
19 ;
20 ; CURRENT FILING DATE: 2003-12-01
21 ;
22 ; PRIORITY APPLICATION NUMBER: 60/429,992
23 ;
24 ; PRIOR FILING DATE: 2002-11-29
25 ;
26 ; NUMBER OF SEQ ID NOS: 14
27 ;
28 ; SOFTWARE: PatentIn version 3.2
29 ;
30 ; SEQ ID NO 1
31 ;
32 ; LENGTH: 529
33 ;
34 ; TYPE: DNA
35 ;
36 ; ORGANISM: Solanum americanum
37 ;
38 ; US-10-725-829-1

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Query Match	100.0%	Score 529;	DB 20;	Length 529;
Best Local Similarity	100.0%	Prod. No. 4.8e-268;		
Matches 529;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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RESULT 2

US-11-093-776-4
Sequence 4, Application US/11093776
Publication No. US20050172356A1
GENERAL INFORMATION:
APPLICANT: Christeller, John Tane
APPLICANT: Sutherland, Paul William
APPLICANT: Murray, Colleen
APPLICANT: Markwick, Ngairie Patricia
APPLICANT: Philip, Bruce Allan
APPLICANT: Malone, Louise Anne
APPLICANT: Burgess, Elisabeth Phyllis
APPLICANT: Phung, Margaret Mary
APPLICANT: The Horticulture and Food Research Institute of
New Zealand Limited
TITLE OF INVENTION: Chimeric Polypeptides Allowing Expression of
FILE REFERENCE: 020829-000100US
CURRENT APPLICATION NUMBER: US/11/093,776
PRIOR FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: US/09/743,690
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: NZ 331002
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: NO PCT/NZ99/00110
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 584
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: potato
OTHER INFORMATION: proteinase inhibitor II (PPI-II/pUC19)
FEATURE:
NAME/KEY: CDS

LOCATION: (1) .. (584)
OTHER INFORMATION: PPI-II/pUC19
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1) .. (212)
OTHER INFORMATION: signal sequence
US-11-093-776-4

Query Match 5.1%; Score 27; DB 24; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 CAATGTTGCTCAGGCTATTAAGGTTG 195
Db 296 CAATGTTGCTCAGGCTATTAAGGTTG 322

RESULT 3

US-10-725-829-12
Sequence 12, Application US/10725829
Publication No. US20040205846A1
GENERAL INFORMATION:
APPLICANT: Chye, Mee Len
APPLICANT: Xu, Zeng-Fu
APPLICANT: Sin, Suk Fong
TITLE OF INVENTION: Genetically Modified Plants with Heterogenous Proteinase Inhibitor
TITLE OF INVENTION: SAPIN2A or SAPIN2B and Methods of Use Thereof for the Inhibitor
FILE REFERENCE: 9661-043-999
CURRENT APPLICATION NUMBER: US/10/725,829
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: 60/429,992
PRIOR FILING DATE: 2002-11-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 56
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Description of artificial sequence: primer
US-10-725-829-12

Query Match 4.0%; Score 21; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ATGGCTGTTCAACAAGTTAGC 25
Db 36 ATGGCTGTTCAACAAGTTAGC 56

RESULT 4

US-10-425-115-103020
Sequence 103020, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 103020
LENGTH: 315
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_25461C.1

US-10-425-115-103020

Query Match

Best Local Similarity 3.8%; Score 20; DB 20; Length 315;
Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

312 CAGNAGGAGAGATGATAATT 331
|||||
140 CAGNAGGAGAGATGATAATT 159

RESULT 5

US-10-282-122A-12113/C

; Sequence 12113, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12113
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Bacteroides fragilis
US-10-282-122A-12113

Query Match

Best Local Similarity 3.8%; Score 20; DB 17; Length 471;
Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

466 TTATCTATCAAAAAATA 485
|||||
176 TTATCTATCAAAAAATA 157

RESULT 6

US-10-725-829-3
; Sequence 3, Application US/10725829

; Publication No. US20040205846A1

GENERAL INFORMATION:

; APPLICANT: Chye, Mee Len
; APPLICANT: Xu, Zeng-Fu
; APPLICANT: Shi, Suk Fong
; TITLE OF INVENTION: Genetically Modified Plants with Heterogenous Proteinase Inhibitor
; TITLE OF INVENTION: SAPIN2B or SAPIN2B and Methods of Use Thereof for the Inhibitor
; TITLE OF INVENTION: of Trypsin- and Chymotrypsin-Like Activities
; FILE REFERENCE: 9661-043-999
; CURRENT APPLICATION NUMBER: US/10/725,829
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/429,992
; PRIOR FILING DATE: 2002-11-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Solanum americanum
US-10-725-829-3

Query Match

Best Local Similarity 3.8%; Score 20; DB 20; Length 692;
Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

170 AATTGTTGCTCAGGCTATA 189
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210 AATTGTTGCTCAGGCTATA 229

RESULT 7

US-09-812-502-1

; Sequence 1, Application US/09812502
; Publication No. US20030027303A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Marilyn A.
; APPLICANT: Atkinson, Angela H.
; APPLICANT: Heath, Robyn L.
; APPLICANT: Clarke, Adrienne E.
; TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
; FILE REFERENCE: 9748B
; CURRENT APPLICATION NUMBER: US/09/812,502
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US/09/431,500
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 08/454,295
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Nicotiana glauca
US-09-812-502-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 10; Length 1104;
Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

224 AATTGGAAGAGAACTGA 243
|||||
1012 AATTGGAAGAGAACTGA 1031

RESULT 8

US-10-164-961-1
; Sequence 1, Application US/10164961
; Publication No. US20030096388A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Marilyn A.
; APPLICANT: Atkinson, Angela H.
; APPLICANT: Heath, Robyn L.

Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164,961
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-164-961-1
Query Match 3.8%; Score 20; DB 14; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 ATTGTGAAGAGAAATCTGA 243
Db 1012 ATTGTGAAGAGAAATCTGA 1031
RESULT 9
US-10-157-622-1
Sequence 1, Application US/10157622
Publication No. US20030129720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
Heath, Robyn L.
Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/157,622
FILING DATE: 29-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-157-622-1
Query Match 3.8%; Score 20; DB 15; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 ATTGTGAAGAGAAATCTGA 243
Db 1012 ATTGTGAAGAGAAATCTGA 1031
RESULT 10
US-10-072-809A-56
Sequence 56, Application US/10072809A
Publication No. US20030217382A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A., Lay, Fung T., Heath, Robyn, L.
TITLE OF INVENTION: Plant-derived molecules and genetic sequences encoding same and
FILE REFERENCE: 18-01
CURRENT APPLICATION NUMBER: US/10/072,809A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: USSN 60/267,271
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 56
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1104)
US-10-072-809A-56
Query Match 3.8%; Score 20; DB 17; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 ATTGTGAAGAGAAATCTGA 243
Db 1012 ATTGTGAAGAGAAATCTGA 1031
RESULT 11
US-11-062-999-56
Sequence 56, Application US/11062999
Publication No. US20050150004A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A., Lay, Fung T., Heath, Robyn, L.
TITLE OF INVENTION: Defensein-encoding nucleic acid molecules derived from Nicotiana

FILE OF INVENTION: uses therefor and transgenic plants comprising same
FILE REFERENCE: 18-01A
CURRENT APPLICATION NUMBER: US/11/062,999
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: USSN 10/072,809
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: USSN 60/267,271
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 56
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1104)
US-11-062-999-56

Query Match 3.8%; Score 20; DB 24; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTTGTGAAGAGATCTGA 243
|||||
DB 1012 ATTTGTGAAGAGATCTGA 1031

RESULT 12
US-10-425-114-36251
Sequence 36251; Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaka, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 36251
LENGTH: 1167
TYPE: DNA
ORGANISM: Zea mays subsp. mexicana
FEATURE:
OTHER INFORMATION: Clone ID: UC-2MROTOSINTE067C12_FLI
US-10-425-114-36251

Query Match 3.8%; Score 20; DB 18; Length 1167;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 GATACACAGATCTTATTC 297
|||||
DB 396 GATACACAGATCTTATTC 415

RESULT 13
US-09-812-502-2
Sequence 2; Application US/09812502
Publication No. US20030027303A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FEATURE: SEQUENCES ENCODING SAME

FILE REFERENCE: 9748B
CURRENT APPLICATION NUMBER: US/09/812,502
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US/09/431,500
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 08/454,295
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1360
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (97)..(1200)
US-09-812-502-2

Query Match 3.8%; Score 20; DB 10; Length 1360;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTTGTGAAGAGATCTGA 243
|||||
DB 1108 ATTTGTGAAGAGATCTGA 1127

RESULT 14
US-10-164-961-2
Sequence 2; Application US/10164961
Publication No. US20030096388A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164,961
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

Search completed: August 22, 2005, 09:42:17
Job time : 4717 secs

NAME/KEY: CDS
LOCATION: 97..1200
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-164-961-2

Query Match 3.8%; Score 20; DB 14; Length 1360;
Best Local Similarity 100.0%; Pred.No.10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 ATTTGTAAGAGAACTCTGA 243
|||||
DB 1108 ATTTGTAAGAGAACTCTGA 1127

RESULT 15
US-10-157-622-2

Sequence 2, Application US/10157622
Publication No. US20030129720A1
GENERAL INFORMATION:

APPLICANT: Anderson, Marilyn A.
Atkinson, Angela H.

Heath, Robyn L.
Clarke, Adrienne E.

TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/157,622

FILING DATE: 29-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/454,295

FILING DATE: 01-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: DIGIGLIO, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9748

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1360 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 97..1200

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-157-622-2

Query Match 3.8%; Score 20; DB 15; Length 1360;
Best Local Similarity 100.0%; Pred.No.10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 ATTTGTAAGAGAACTCTGA 243
|||||
DB 1108 ATTTGTAAGAGAACTCTGA 1127

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OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 00:38:16 ; Search time 148 Seconds

(without alignments)
5848.584 Million cell updates/sec

Title: US-10-725-829-1

Perfect score: 529
Sequence: 1 cataatgcgttcacaaag.....ctgaatcgtagctatttg 529

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	3.8	1104	3	US-08-454-295-1
2	20	3.8	1104	3	US-09-431-500A-1
3	20	3.8	1104	3	US-09-431-498-1
4	20	3.8	1104	3	US-09-431-499-1
5	20	3.8	1104	4	US-08-812-502B-1
6	20	3.8	1360	3	US-08-454-295-2
7	20	3.8	1360	3	US-09-431-500A-2
8	20	3.8	1360	3	US-09-431-498-2
9	20	3.8	1360	3	US-09-431-499-2
10	20	3.8	1360	4	US-08-812-502B-2
11	19	3.6	432	4	US-08-248-796A-7188
12	19	3.6	4066	4	US-09-710-279-4327
13	19	3.6	9900	4	US-09-949-016-13392
14	18	3.4	601	4	US-09-949-016-13858
15	18	3.4	601	4	US-09-949-016-23859
16	18	3.4	601	4	US-09-949-016-197801
17	18	3.4	601	4	US-09-949-016-197802
18	18	3.4	601	4	US-09-949-016-197808
19	18	3.4	601	4	US-09-949-016-197849
20	18	3.4	1025	4	US-09-270-767-4982
21	18	3.4	1025	4	US-09-270-767-20264
22	18	3.4	2907	4	US-09-620-312D-511
23	18	3.4	9527	4	US-09-949-016-13979
24	18	3.4	51927	4	US-09-949-016-17347
25	18	3.4	51927	4	US-09-949-016-17348
26	18	3.4	73853	4	US-09-949-016-12029
27	18	3.4	580073	4	US-08-545-528D-1

C 28	18	3.4	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
C 29	18	3.4	1664976	4	US-09-692-570-1	Sequence 1, Appl1
C 30	18	3.4	1830121	4	US-09-557-884-1	Sequence 1, Appl1
C 31	18	3.4	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
C 32	17	3.2	339	4	US-09-248-796A-55971	Sequence 5971, Ap
C 33	17	3.2	517	4	US-09-640-211A-1352	Sequence 1352, Ap
C 34	17	3.2	601	4	US-09-949-016-67034	Sequence 67034, A
C 35	17	3.2	601	4	US-09-949-016-78439	Sequence 78439, A
C 36	17	3.2	601	4	US-09-949-016-146757	Sequence 146757, A
C 37	17	3.2	601	4	US-09-949-016-150280	Sequence 150280, A
C 38	17	3.2	601	4	US-09-949-016-190173	Sequence 190173, A
C 39	17	3.2	601	4	US-09-949-016-190174	Sequence 190174, A
C 40	17	3.2	601	4	US-09-949-016-190175	Sequence 190175, A
C 41	17	3.2	601	4	US-09-949-016-190176	Sequence 190176, A
C 42	17	3.2	601	4	US-09-949-016-190177	Sequence 190177, A
C 43	17	3.2	601	4	US-09-949-016-199232	Sequence 199232, A
C 44	17	3.2	601	4	US-09-949-016-199233	Sequence 199233, A
C 45	17	3.2	601	4	US-09-949-016-199234	Sequence 199234, A

ALIGNMENTS

RESULT 1
US-08-454-295-1
Sequence 1, Application US/08454295
Patent No. 6031087
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Arlene E.
TITLE OR INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-295-1
Query Match 3.8%; Score 20; DB 3; Length 1104;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

DB 1012 ATTGTGAAGAGAACTCGA 1031

RESULT 2

US-09-431-500A-1
Sequence 1, Application US/09431500A
Patent No. 6261821
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B
CURRENT APPLICATION NUMBER: US/09/431,500A
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 08/454,295
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
US-09-431-500A-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 3; Length 1104;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTCGA 243

DB 1012 ATTGTGAAGAGAACTCGA 1031

RESULT 3

US-09-431-498-1
Sequence 1, Application US/09431498
Patent No. 6440727
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,498
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,295
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-431-498-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 3; Length 1104;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTCGA 243

DB 1012 ATTGTGAAGAGAACTCGA 1031

RESULT 4

US-09-431-499-1
Sequence 1, Application US/09431499
Patent No. 6451573
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-431-499-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 3; Length 1104;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTCGA 243

Db 1012 ATTGTGAAGAGAAATCTGA 1031

RESULT 5
US-09-812-502B-1
Sequence 1, Application US/09812502B

Patent No. 6806074
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B2
CURRENT APPLICATION NUMBER: US/09/812,502B
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/431,500
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
US-09-812-502B-1

Query Match 3.8%; Score 20; DB 4; Length 1104;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAAATCTGA 243
Db 1012 ATTGTGAAGAGAAATCTGA 1031

RESULT 6
US-08-454-295-2
Sequence 2, Application US/08454295
Patent No. 6031087
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:

LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 97..1200
US-08-454-295-2

Query Match 3.8%; Score 20; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAAATCTGA 243
Db 1108 ATTGTGAAGAGAAATCTGA 1127

RESULT 7
US-09-431-500A-2
Sequence 2, Application US/09431500A
Patent No. 6261821
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B
CURRENT APPLICATION NUMBER: US/09/431,500A
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 08/454,295
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1360
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (97)..(1200)
US-09-431-500A-2

Query Match 3.8%; Score 20; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAAATCTGA 243
Db 1108 ATTGTGAAGAGAAATCTGA 1127

RESULT 8
US-09-431-498-2
Sequence 2, Application US/09431498
Patent No. 6440727
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,498
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,295
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 97..1200
US-09-431-498-2

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 1360;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTTGA 243
DB 1108 ATTGTGAAGAGAACTTGA 1127

RESULT 9
US-09-431-499-2
Sequence 2, Application US/09431499
Patent No. 6451573
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF
TITLE OF INVENTION: AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 97..1200
US-09-431-499-2

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 1360;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTTGA 243
DB 1108 ATTGTGAAGAGAACTTGA 1127

RESULT 10
US-09-812-502B-2
Sequence 2, Application US/09812502B
Patent No. 6806074
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B2
CURRENT APPLICATION NUMBER: US/09/812,502B
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/431,500
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1360
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (97)..(1200)
US-09-812-502B-2

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 1360;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTTGA 243
DB 1108 ATTGTGAAGAGAACTTGA 1127

RESULT 11
US-09-248-796A-7188
Sequence 7188, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
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```

: CURRENT APPLICATION NUMBER: US/09/248,796A
: CURRENT FILING DATE: 1998-02-12
: PRIOR APPLICATION NUMBER: US 60/074,725
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: US 60/096,409
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 28208
: SEQ ID NO 7188
: LENGTH: 432
: TYPE: DNA
: ORGANISM: Candida albicans
US-09-248-796A-7188

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Query Match      3.6%;   Score 19;   DB 4;   Length 432;
Best Local Similarity 100.0%;   Pred. No. 9.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	42	TTGTTCTTGATGATGTT	60
Db	170	TTGTTCTTGATGATGTT	188

RESULT 12
 US-09-710-279-4327/C
 ; Sequence 4327, Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUS480US
 ; CURRENT APPLICATION NUMBER: US/09/710,279
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4327
 ;
 ; LENGTH: 4066
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ;
 ; US-09-710-279-4327

Query Match	3.6%	Score 19	DB 4	Length 4066
Best Local Similarity	100.0%	Pred. No. 10		
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

OY 185 TATAAGGTTGCACTATT 203
 |||||
Db 1674 TATAAGGGTTCACACTATT 1656

```

1      RESULT 13
2      US-09-949-016-13392/C
3      ; Sequence 13392, Application US/09949016
4      ; Patent No. 6812339
5      ; GENERAL INFORMATION:
6      ; APPLICANT: VENTER, J. Craig et al.
7      ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
8      ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
9      ; FILE REFERENCE: C1001307
10     ; CURRENT APPLICATION NUMBER: US/09/949, 016
11     ; CURRENT FILING DATE: 2000-04-14
12     ; PRIOR APPLICATION NUMBER: 60/241,755
13     ; PRIOR FILING DATE: 2000-10-20
14     ; PRIOR APPLICATION NUMBER: 60/237,768
15     ; PRIOR FILING DATE: 2000-10-03
16     ; PRIOR APPLICATION NUMBER: 60/231,498
17     ; PRIOR FILING DATE: 2000-09-08
18     ; NUMBER OF SEQ ID NOS: 207012
19     ; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 13392
; LENGTH: 9900
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13392

```

Query Match	3.6%	Score 19	DB 4	Length 9900
Best Local Similarity	100.0%	Pred. No. 10		
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 236 GAATCTGACCCCTAGAACC 254
|||||
Db 9716 GAATCTGACCCCTAGAACC 9698

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RESULT 14
US-09-949-016-23858/c
: Sequence 23858, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 23858
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-23858

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Query Match	3.4%	Score 18	DB 4	length 601
Best Local Similarity	100.0%	Pred. No.	32	
Matches 18	Conservative	0	Mismatches	0
		0	Indels	0
			Gaps	0

QY 404 GTCTGTGAAGGAGAGT 421
|||
Db 169 GTCTGTGAAGGAGAGT 152

```

RESULT 15
US-09-949-016-23859/C
; Sequence 23859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23859
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-23859

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Query Match 3.4%; Score 18; DB 4; Length 601;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 404 GTCTGTGAAGAGAGAGT 421
|||||
Db 513 GTCTGTGAAGAGAGAGT 496

Search completed: August 22, 2005, 03:59:55
Job time : 152 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 02:23:22 ; Search time 2491 Seconds

(without alignments)
10290.168 Million cell updates/sec

Title: US-10-725-829-1

Perfect score: 529
Sequence: 1 cataatggcgttcacaaag.....ctgtaatgctgacttattcg 529

Scoring table: OLIGO_NTC
Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb ba:*
2: gb htg:*
3: gb_in:*
4: gb_om:*
5: gb_cv:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	529	100.0	529	8	AF174381	AF174381 Solanum a
2	38	7.2	1573	8	STPRINBEG	Z12824 S. tuberosum
3	35	6.6	859	8	AB110700	AB110700 Lycopersi
4	35	6.6	660	8	TOMWIP11	K03291 Tomato leaf
5	35	6.6	684	8	AY007240	AY007240 Lycopersi
6	35	6.6	687	8	AY422686	AY422686 Solanum n
7	35	6.6	1670	8	AY129402	AY129402 Lycopersi
8	35	6.6	1776	8	BT013250	BT013250 Lycopersi
9	27	5.1	364	8	STPIN2	X78275 S. tuberosum
10	27	5.1	2068	8	STU45450	U45450 Solanum tub
11	27	5.1	2330	8	STPRIN11	Z13992 S. tuberosum
12	26	4.9	512	8	STPRIN11	X03778 Potato (Sol
13	26	4.9	554	8	STPRIN11	X03779 Potato (Sol
14	26	4.9	666	8	POTPINHB	X73519 Solanum tub
15	26	4.9	838	8	STPIN2W	X99035 S. tuberosum
16	26	4.9	1241	8	POTL1KA	M15186 S. tuberosum
17	26	4.9	1695	8	STPRIN2G	Z12753 S. tuberosum
18	26	4.9	1914	8	STPI2G	X04118 Potato gene
19	25	4.7	764	8	AF221097	AF221097 Capsicum

20	4.7	836	8	AF039398	AF039398 Capsicum
21	4.3	482	8	AY247794	AY247794 Solanum p
22	4.3	580	8	AY517498	AY517498 Solanum p
23	4.3	766	8	LECEV157G	X94946 L. esculentu
24	4.3	1274	8	NTPROTINH	Z29537 N. tabacum (
25	4.0	89779	8	AB005234	AB005234 Arabidops
26	4.0	170076	2	AC117720	AC117720 Mus muscu
27	4.0	175045	10	AL590418	AL590418 Mouse DNA
28	4.0	181805	10	AL670660	AL670660 Mouse DNA
29	4.0	185737	2	AC125447	AC125447 Mus muscu
30	4.0	233766	2	AC113755	AC113755 Rattus no
31	4.0	239081	2	AC108242	AC108242 Rattus no
32	4.0	243770	2	AC123492	AC123492 Rattus no
33	3.8	532	8	AF209709	AF209709 Solanum a
34	3.8	532	8	BT013127	BT013127 Lycopersi
35	3.8	866	8	AF105340	AF105340 Nicotiana
36	3.8	1104	6	E54394	E54394 Transgenic
37	3.8	1104	6	AR224421	AR224421 Sequence
38	3.8	1104	6	AR230262	AR230262 Sequence
39	3.8	1332	8	AY297103	AY297103 Nicotiana
40	3.8	1332	8	AF205852	AF205852 Nicotiana
41	3.8	1342	8	NAU08219	U08219 Nicotiana a
42	3.8	1360	6	E54395	E54395 Transgenic
43	3.8	1360	6	AR224422	AR224422 Sequence
44	3.8	1360	6	AR230263	AR230263 Sequence
45	3.8	1414	8	AY426751	AY426751 Nicotiana

ALIGNMENTS

RESULT 1
AF174381
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITL
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITL
JOURNAL
FEATURES
source
gene
CDS

AF174381 529 bp mRNA linear PLN 15-JAN-2002
Solanum americanum proteinase inhibitor IIA (PIN2a) mRNA, complete cds.
AF174381.1 GI:17221674
Solanum americanum
Solanum americanum
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 529)
Xu, Z.-F., Qi, W.-Q., Ouyang, X.-Z., Yeung, E. and Che, M.-L.
A proteinase inhibitor II of Solanum americanum is expressed in phloem
Plant Mol. Biol. 47 (6), 727-738 (2001)
21643209
MEDLINE
11785934
PUBMED
2 (bases 1 to 529)
Che, M.-L. and Xu Z.-F.
Direct Submission
Submitted (01-AUG-1999) Department of Botany, The University of Hong Kong, Pokfulam Road, Hong Kong, China
Location/Qualifiers
1..529
/organism="Solanum americanum"
/mol_type="mRNA"
/db_xref="taxon:109975"
1..529
/gene="PIN2a"
5..1451
/gene="PIN2a"
/codon_start=1
/product="proteinase inhibitor IIA"
/protein_id="AA136458.1"
/translation="MAVHKVSLACLVLVGMWFLAKVDAACTRCGHFSGYICPR
SEGSPQKICTNCGYVSAKGLICGSESDPNPKCTECFQIAYSKCPR
SEGMKIIKPTGCTCTCGYGCYVDPQGDFFVCEGSESEPKTAYF"
ORIGIN

Query Match 100.0%; Score 529; DB 8; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1.1e-284;
 Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTAAGGCTGTTCACAAAGTTAGCTTCCCTTGGCTTCTGCTTCTTGGATGATGTT 60
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 DB 1 CATTAAGGCTGTTCACAAAGTTAGCTTCCCTTGGCTTCTGCTTCTTGGATGATGTT 60
 61 TCTACTTGGCAACATGTTGATGCCAAGGCTTGTACTAGAGATGCTGATTTTGA 120
 |||||
 DB 61 TCTACTTGGCAACATGTTGATGCCAAGGCTTGTACTAGAGATGCTGATTTTGA 120
 121 TGGCATATGCCCCAGCTTCAGAGAGAGTCCCCCAAAACCTATATGACCAATGTTGCTC 180
 |||||
 DB 121 TGGCATATGCCCCAGCTTCAGAGAGAGTCCCCCAAAACCTATATGACCAATGTTGCTC 180
 181 AGGCTTAAAGGCTTGCACCTTATACAGTGTCTAAAGAGATTTTGTGTAAGAGATTC 240
 |||||
 DB 181 AGGCTTAAAGGCTTGCACCTTATACAGTGTCTAAAGAGATTTTGTGTAAGAGATTC 240
 241 TGACCTTGAACACCAAAAGATTGTACCTTCGATGATGATACAGATGCTTATTCAA 300
 |||||
 DB 241 TGACCTTGAACACCAAAAGATTGTACCTTCGATGATGATACAGATGCTTATTCAA 300
 301 ATGTCTCTGTTGAGAGAGAAAGATGATTAATTAACCACTGATGACCACTTGTGAC 360
 |||||
 DB 301 ATGTCTCTGTTGAGAGAGAAAGATGATTAATTAACCACTGATGACCACTTGTGAC 360
 361 GGGCTATCAGGGTGTCTACTATTTCATCAAGATGATGATTTTGTCTGTAAGAGAGAG 420
 |||||
 DB 361 GGGCTATCAGGGTGTCTACTATTTCATCAAGATGATGATTTTGTCTGTAAGAGAGAG 420
 421 TCCTGAACCAAGACCACTGCTTATTTCTATCAATCATATGTTGATTCATCAAAAA 480
 |||||
 DB 421 TCCTGAACCAAGACCACTGCTTATTTCTATCAATCATATGTTGATTCATCAAAAA 480
 481 AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
 |||||
 DB 481 AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529

RESULT 2
 STRIPINSG 1573 bp DNA linear PLN 11-MAY-1995
 LOCUS 212824
 DEFINITION S.tuberosum protease inhibitor pseudogene.
 ACCESSION 212824
 VERSION 1
 KEYWORDS protease inhibitor.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 1573)
 Cho, Y., Moon, Y. and Lee, J.S.
 PRIMARY structure of two protease inhibitor II genes closely
 linked in the potato genome
 Hanguk Saengwhakhoe Chi 23, 214-220 (1990)
 2 (bases 1 to 1573)
 Lee, J.S.
 DIRECT Submission
 Submitted (19-JUN-1992) Jong S. Lee, Molecular Biology, Seoul
 National University, Shinrim Dong, Kwanak-Gu, Seoul, 151-742,
 Republic of Korea
 Multiple conflicts with Keil et al., (1986) Nucl. Acids Res.
 14,5641-5650.
 FEATURES
 source 1..1573
 Location/Qualifiers
 /organism="Solanum tuberosum"
 /mol_type="genomic DNA"
 /cultiivar="Russet Burbank"
 /db_xref="taxon:4113"

CAT signal 153..156
 TATA signal 229..234
 CDS 309..925
 /note="protease inhibitor"

ORIGIN polyA_signal
 1269..1274

Query Match 7.2%; Score 38; DB 8; Length 1573;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 ACCAATGTTGCTCAGGCTATAAGGCTTGCAACTATTA 204
 |||||
 DB 648 ACCAATGTTGCTCAGGCTATAAGGCTTGCAACTATTA 685

RESULT 3
 AB110700 559 bp DNA linear PLN 28-MAY-2003
 LOCUS
 DEFINITION Lycopersicon esculentum gene for protease inhibitor II, complete
 cds.
 ACCESSION AB110700
 VERSION AB110700.1 GI:31088241
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1
 Wada, M., Matsuda, Y., Fujita, K., Nanjo, A., Kakutani, K., Nonomura, T.,
 Matsuda, Y. and Toyoda, H.
 Mature mRNAs in targeted single cells can be amplified by RT-PCR of
 nucleus-free cytosolic contents sucked up with micropipette

JOURNAL 2 (bases 1 to 559)
 REFERENCE Nanjo, A., Wada, M., Fujita, K., Sameshima, T., Kakutani, K.,
 Nonomura, T., Matsuda, Y. and Toyoda, H.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAY-2003) Yoshinori Matsuda, Kinki University,
 Laboratory of Plant Pathology and Biotechnology Faculty of
 Agriculture, 3327-204 Nakamachi, Nara, Nara 631-8505, Japan
 (E-mail: ymatsuda@nara.kindai.ac.jp, Tel: 81-742-43-1511 (ex. 3111),
 Fax: 81-742-43-1155)

FEATURES
 source 1..559
 Location/Qualifiers
 /organism="Lycopersicon esculentum"
 /mol_type="genomic DNA"
 /cultiivar="MoneyMaker"
 /db_xref="taxon:4081"
 join(2..53,165..559)
 /codon_start=1
 /product="protease inhibitor II"
 /protein_id="BAC76901.1"
 /db_xref="GI:31088242"

CDS
 1
 /translation="MAVKEVNFVAIVLIVGMPVYVDAKATRECGNIGFGICPRSE
 GSPINPICNCSGKGCNYSREKFLCEBSIDPKRNACTFENDPPIAASRCRRO
 GKSILYFGCTTCCTGKCYGKCYRFGDGFVEGSDERKANNPYPM"

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 559;
 Best Local Similarity 100.0%; Pred. No. 8e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ATGTGATGCCAAGGCTGTACTAGAGATGCT 109
 |||||
 DB 177 ATGTGATGCCAAGGCTGTACTAGAGATGCT 211

RESULT 4
 TOMMIPIT

LOCUS TOMWIP1I 660 bp mRNA linear PLN 27-APR-1993
 DEFINITION Tomato leaf wound-induced proteinase inhibitor II mRNA, complete cds.
 ACCESSION K03291
 VERSION K03291.1 GI:170521
 KEYWORDS protease inhibitor; wound-induced protease inhibitor.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 Graham, J.S., Pearce, G., Merryweather, J., Tiltan, K., Ericsson, L.H. and Ryan, C.A.
 Wound-induced proteinase inhibitors from tomato leaves. II. The cDNA-decoded primary structure of pre-inhibitor II
 J. Biol. Chem. 260 (11), 6561-6564 (1985)
 MEDLINE 85207658
 PUBMED 3838986
 COMMENT Original source text: Tomato (L. esculentum L. var. Bonnie Best) wounded leaf, cDNA to mRNA, clone pTI-24.
 A 10 bp palindrome identical to the one following the TOMWIP1 cds (see separate entry) begins at position 586 [1]. A polyadenylation signal is present at position 638-643 [1].
 A printed copy of this sequence was kindly provided by C.A. Ryan (18-SEP-1985).

FEATURES
 source
 1..660
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 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /db_xref="taxon:4081"
 <1..660
 /product="WIP1I mRNA"
 49..495
 /note="wound-induced proteinase inhibitor II prepeptide"
 /codon_start=1
 /protein_id="AA34201.1"
 /db_xref="GI:170522"
 /translation="MAVHKEVNFVAVLLIVLGMFLYDAACTRECNLGGICPRSE
 GSPNPICINCCSGYKGCYNYSFGKFCESBSPKPNACTPCDNLNAYSRCPSO
 GKSLIYPTGCTCTCTGKCYFGKDKFVCEGSDPKANMYPVM"
 49..123
 /note="wound-induced proteinase inhibitor II signal
 peptide"
 124..492
 /product="wound-induced proteinase inhibitor II mature
 peptide"
 mat_peptide
 279 bp upstream of Sau3A site.
 ORIGIN
 Query Match 6.6%; Score 35; DB 8; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 75 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 109
 |||
 113 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 147

RESULT 5
 AY007240 684 bp DNA linear PLN 02-JAN-2001
 LOCUS Lycopersicon esculentum proteinase inhibitor II gene, complete cds.
 ACCESSION AY007240
 VERSION AY007240.1 GI:12007535
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 Xie, X. and Wu, N.
 Isolation of tomato proteinase inhibitor II gene and analysis of

JOURNAL its structure
 REFERENCE 2 (bases 1 to 684)
 AUTHORS Xie, X. and Wu, N.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-2000) Plant Developmental Molecular Biology,
 Institute of Developmental Biology, Chinese Academy of Sciences,
 Nanyitiao No.3, Zhongguancun, Haidian District, Beijing 100080,
 China

FEATURES
 source
 1..684
 /organism="Lycopersicon esculentum"
 /mol_type="genomic DNA"
 /db_xref="taxon:4081"
 join(<9..60,170..564)
 /product="proteinase inhibitor II"
 join(9..60,170..564)
 /codon_start=1
 /product="proteinase inhibitor II"
 /protein_id="AA012170.1"
 /db_xref="GI:12007536"
 /translation="MAVHKEVNFVAVLLIVLGMFLYDAACTRECNLGGICPRSE
 GSPNPICINCCSGYKGCYNYSFGKFCESBSPKPNACTPCDNLNAYSRCPSO
 GKSLIYPTGCTCTCTGKCYFGKDKFVCEGSDPKANMYPVM"

ORIGIN
 Query Match 6.6%; Score 35; DB 8; Length 684;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 75 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 109
 |||
 182 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 216

RESULT 6
 AY422686 687 bp mRNA linear PLN 18-MAY-2004
 LOCUS Solanum nigrum proteinase inhibitor 2b precursor (PIN2b) mRNA,
 complete cds.
 ACCESSION AY422686
 VERSION AY422686.1 GI:40036963
 KEYWORDS
 SOURCE Solanum nigrum (black nightshade)
 ORGANISM Solanum nigrum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
 Schmidt, D.D., Kessler, A., Kessler, D., Schmidt, S., Lim, M., Gase, K. and Baldwin, I.T.
 Solanum nigrum: a model ecological expression system and its tools
 Mol. Ecol. 13 (5), 981-995 (2004)
 15078438
 2 (bases 1 to 687)
 Schmidt, D.D., Gase, K. and Baldwin, I.T.
 Direct Submission
 Submitted (25-SEP-2003) Molecular Ecology, Max Planck Institute for
 Chemical Ecology, Hans-Knoell-Strasse 8, Jena D-07745, Germany

FEATURES
 source
 1..687
 /organism="Solanum nigrum"
 /mol_type="mRNA"
 /db_xref="taxon:4112"
 1..687
 /gene="PIN2b"
 28..486
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 /product="proteinase inhibitor 2b precursor"
 /protein_id="AA037362.1"
 /db_xref="GI:40036964"
 /translation="MAVHKEVNSLAVLVGLFLFVSAIKHVDAPCTRECNLGGIC

sig_peptide

ICPSSGSGPENPCTNCCSGYKGCNTYANGTICRSGSSDPKPNTPCPLXCDIDAYS
KCPSSGSGTITVPTGCTTCTCTGKCYFSEKSEFPVCEGSEIEPNVINSQ
28..120
/gene="PIN2b"
/evidence=not_experimental

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 687;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 AATTGTTGCTCAGGCTTAAGGCTTGCACTATTA 204
|||||
DB 205 AATTGTTGCTCAGGCTTAAGGCTTGCACTATTA 239

RESULT 7
LOCUS AY129402 1670 bp DNA linear PLN 16-JUN-2004
DEFINITION Lycopersicon esculentum proteinase inhibitor II gene, complete cds.
ACCESSION AY129402
VERSION AY129402.1 GI:33413549
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1670)
Zhang, H.Y., Xie, X.Z., Xu, Y.Z. and Wu, N.H.
Isolation and functional assessment of a tomato proteinase
inhibitor II gene
Plant Physiol. Biochem. 42 (5), 437-444 (2004)
2 (bases 1 to 1670)
15191748
JOURNAL
PUBMED
AUTHORS Zhang, H., Xie, X., Wu, N. and Huang, M.
TITLES Direct Submission
SUBMITTED (08-JUL-2002) Institute of Genetics and Developmental
Biology, Chinese Academy of Sciences, Nanyitiao No.3 Zhongguancun,
Beijing 2707, China
LOCATION/Qualifiers

FEATURES
source
1..1670
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/db_xref="taxon:4081"
/join(<995..1046,1156..>1550)
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/protein_id="AN05016.1"
/db_xref="GI:33413550"
/translation="MAVHKVEVFVAVLLVILGFLVYDAKACTREGCNLGFICPSE
GSPINPCINCGSGYKGCNTYANGTICRSGSSDPKPNTPCPLXCDIDAYS
KCPSSGSGTITVPTGCTTCTCTGKCYFSEKSEFPVCEGSEIEPNVINSQ
GKSLITPTGCTTCTCTGKCYFSEKSEFPVCEGSEIEPNVINSQ"

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 1670;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 109
|||||
DB 1168 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 1202

RESULT 8
LOCUS BT013250 1776 bp mRNA linear PLN 11-MAY-2004
DEFINITION Lycopersicon esculentum clone 134756F, mRNA sequence.
ACCESSION BT013250
VERSION BT013250.1 GI:47104665
KEYWORDS FLI_CDNA.

SOURCE

Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1776)
Kirkness, E.F., Wang, W. and Vazeille, A.
Direct Submission
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA
LOCATION/Qualifiers

ORGANISM

REFERENCE

1..1776
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
/clone="134756F"
/issue_type="mixed elicitor"
/note="TMECD39"

FEATURES

source
1..1776
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
/clone="134756F"
/issue_type="mixed elicitor"
/note="TMECD39"

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 1776;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 109
|||||
DB 108 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 142

RESULT 9

STPIN2 584 bp DNA linear PLN 14-JUL-1995
LOCUS STPIN2 S.tuberosum (Arran Banner) pin2-CM7 gene.
DEFINITION X78275
ACCESSION X78275.1 GI:467609
VERSION pin2 gene; protease inhibitor II.
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1
Murray, C. and Christeller, J.T.
Genomic nucleotide sequence of a proteinase inhibitor II gene
Plant Physiol. 106 (4), 1681 (1994)
95148744
MEDLINE
PUBMED
AUTHORS Murray, C.
TITLES Direct Submission
SUBMITTED (17-MAR-1994) C. Murray, The Horticultural and Food
Research Institute of New Zealand Ltd., Batchelar Research Centre,
Tennent Drive, Private Bag 11 030, Palmerston North, NEW ZEALAND
LOCATION/Qualifiers

FEATURES

source
1..584
/organism="Solanum tuberosum"
/mol_type="genomic DNA"
/cultivar="Arran Banner"
/db_xref="taxon:4113"
/cissue_type="leaf"
/join(1..52,172..584)
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/join(1..52,172..584)
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/product="proteinase inhibitor II"
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/db_xref="GI:467610"
/db_xref="GOA:Q43652"
/translation="MDVHKVEVFVAVLLVILGFLVYDAKACTREGCNLGFICPSE
GSPINPCINCGSGYKGCNTYANGTICRSGSSDPKPNTPCPLXCDIDAYS
KCPSSGSGTITVPTGCTTCTCTGKCYFSEKSEFPVCEGSEIEPNVINSQ
RPHSGKSLITPTGCTTCTCTGKCYFSEKSEFPVCEGSEIEPNVINSQ"

Matches	27; Conservative	0; Mismatches	0; Indels	0; Gaps	0
Qy	169	CAATTGTTGCTCAGGCTATAAGGGTTG	195		
Db	1329	CAATTGTTGCTCAGGCTATAAGGGTTG	1355		
RESULT 11					
LOCUS	STP11R11	2330 bp	DNA	linear	PLN 11-MAY-1995
DEFINITION	S.tuberosum proteinase inhibitor II.				
ACCESSION	Z13992				
VERSION	Z13992.1	GI:21555			
KEYWORDS	proteinase inhibitor II.				
SOURCE	Solanum tuberosum (potato)				
ORGANISM	Solanum tuberosum				
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.				
AUTHORS	1 (bases 1 to 2330)				
TITLE	Choi, Y., Kim, J.W. and Lee, J.S.				
JOURNAL	Characterization of a potato proteinase inhibitor II gene that is expressed constitutively in transgenic tobacco plants				
REFERENCE	Mol. Cells				
AUTHORS	2 (bases 1 to 2330)				
TITLE	Lee, J.S.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (01-JUL-1992) Jong S. Lee, Molecular Biology, Seoul National University, Shinrim dong, Kwanak-Gu, Seoul, 151-742, Republic of Korea				
FEATURES					
source	1..2330				
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	/cultivar="Russet Burbank"				
	/db_xref="taxon:4113"				
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	966..1012				
	join(1013..1064,1178..1569)				
	/codon_start=1				
	/product="proteinase inhibitor II"				
	/protein_id="CAA78383.1"				
	/db_xref="GI:21556"				
	/db_xref="Gene:Q41489"				
	/db_xref="UniProt/Swiss-Prot:Q41489"				
	/translation="MAVHKVESVAYLILYLGMEFLYVDALGCTKKEGNLFGICPRSE				
	GSPNPICINCCSGYKGCNYYSAFGRFICGSDLPKPKACPLACPDNINIAYSRCPRSE				
	GKSLIPTGCTTCTTGKGYFTGNGKFCVCGESDPEKPYMSTA"				
	1013..1064				
	/number=1				
	1178..1569				
	/number=2				
	1702..11707				
ORIGIN					
polyA_signal					
Query Match	5.1%; Score 27; DB 8; Length 2330;				
Best Local Similarity	100.0%; Pred. No. 0.0023;				
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	169	CAATTGTTGCTCAGGCTATAAGGGTTG	195		
Db	1284	CAATTGTTGCTCAGGCTATAAGGGTTG	1310		
RESULT 12					
LOCUS	STP11R11	512 bp	RNA	linear	PLN 12-SEP-1993
DEFINITION	Potato (Solanum tuberosum) mRNA 1 for proteinase inhibitor II.				
ACCESSION	X03778				
VERSION	X03778.1	GI:21523			
KEYWORDS	protease inhibitor.				
SOURCE	Solanum tuberosum (potato)				
ORGANISM	Solanum tuberosum				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

1 (bases 1 to 512)
Sanchez-Serrano, J., Schmidt, R., Schell, J., and Willmitzer, L.
Nucleotide sequence of proteinase inhibitor II encoding cDNA of potato (Solanum tuberosum) and its mode of expression
Mol. Gen. Genet. 203, 15-20 (1986)
Data kindly reviewed (15-JUN-1986) by J. Sanchez-Serrano.
Location/Qualifiers
1. 512

source
/organism="Solanum tuberosum"
/mol_type="mRNA"
/db_xref="taxon:4113"
48. 512
/note="unnamed protein product; put. proteinase inhibitor II (aa 1-154)"
/codon_start=1
/protein_id="CAA27408.1"
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/db_xref="GOA:P01080"
/translation="MDVHKENVFVAVLLIVLGLVLSAMEHVDAACTLRGNGLFGICPRSGSPENRICNCCAGYKANGAFICGSDPKPKPCPCNDPHIAYSFKPRSEKSLIYPTGCTTCTGCTGKCYFKNGKFCVGESEDEPRANMYPAM"

ORIGIN

Query Match 4.9%; Score 26; DB 8; Length 512;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ATATGCCACGTTCCAGAGGAAGTCC 150
|||||
180 ATATGCCACGTTCCAGAGGAAGTCC 205

RESULT 13
STPIN1R2 554 bp mRNA linear PLN 12-JUL-1995
LOCUS Potato (Solanum tuberosum) mRNA 2 for proteinase inhibitor II.
DEFINITION X03779
X03779.1 GI:21525
KEYWORDS protease inhibitor.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 554)
Sanchez-Serrano, J., Schmidt, R., Schell, J., and Willmitzer, L.
Nucleotide sequence of proteinase inhibitor II encoding cDNA of potato (Solanum tuberosum) and its mode of expression
Mol. Gen. Genet. 203, 15-20 (1986)
Data kindly reviewed (15-JUN-1986) by J. Sanchez-Serrano.
Location/Qualifiers
1. 554
/organism="Solanum tuberosum"
/mol_type="mRNA"
/db_xref="taxon:4113"
41. 382
/note="unnamed protein product; put. proteinase inhibitor II (aa 29-154) (1 is 3rd base in codon)"
/codon_start=2
/protein_id="CAA27409.1"
/db_xref="GI:829292"
/db_xref="GOA:O82735"
/db_xref="UniProt/TREMBL:O82735"
/translation="VDAACTLRGNGLFGICPRSGSPENRICNCCAGYKANGAFICGSDPKPKPCPCNDPHIAYSFKPRSEKSLIYPTGCTTCTGCTGKCYFKNGKFCVGESEDEPRANMYPAM"
517. 523
/note="put. polyA signal"
554

misc_feature
polyA_site

/note="polyA site"

Query Match 4.9%; Score 26; DB 8; Length 554;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ATATGCCACGTTCCAGAGGAAGTCC 150
|||||
50 ATATGCCACGTTCCAGAGGAAGTCC 75

RESULT 14
POTPINHB 666 bp mRNA linear PLN 28-NOV-1994
LOCUS Solanum tuberosum proteinase inhibitor II mRNA, complete cds.
DEFINITION L37519
L37519.1 GI:576528
VERSION double-headed proteinase inhibitor; proteinase inhibitor II.
KEYWORDS
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 666)
Jongsma, W.A., Bakker, P.L., Stiekema, W.J. and Bosch, D.D.
Phage display of a double-headed proteinase inhibitor: Analysis of the binding domains of potato proteinase inhibitor II
Plant Mol. Biol. (1995) in press
Original source text: Solanum tuberosum (strain Bintje) tuber cDNA to mRNA.
Location/Qualifiers
1. 666
/organism="Solanum tuberosum"
/mol_type="mRNA"
/strain="Bintje"
/db_xref="taxon:4113"
/clone="p303.S1"
/tissue_type="tuber"
34. 498
/note="putative"
/codon_start=1
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/protein_id="AA53276.1"
/db_xref="GI:576529"
/translation="MAVKEVNFVAVLLIVLGLVLSAMEHVDAACTLRGNGLFGICPRSGSPENRICNCCAGYKANGAFICGSDPKPKPCPCNDPHIAYSFKPRSEKSLIYPTGCTTCTGCTGKCYFKNGKFCVGESEDEPRANMYPAM"

FEATURES
source

CDS

Query Match 4.9%; Score 26; DB 8; Length 666;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 125 ATATGCCACGTTCCAGAGGAAGTCC 150
|||||
166 ATATGCCACGTTCCAGAGGAAGTCC 191

RESULT 15

STPIN2W 838 bp mRNA linear PLN 05-AUG-1997
LOCUS S. tuberosum mRNA for pin2 gene, wound induced.
DEFINITION X99095
X99095.1 GI:1431616
VERSION pin2 gene.
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS
Dammann, C., Rojo, E. and Sanchez-Serrano, J.J.

TITLE Abscissic acid and jasmonic acid activate wound-inducible genes in potato through separate organ-specific signal transduction pathways
JOURNAL Plant J. 11, 101-110 (1997)
REFERENCE 2 (bases 1 to 838)
AUTHORS Dammann, C.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-1996) C. Dammann, Centro Nacional de Biotecnología, Plant Genetics, Campus de Cantoblanco, 28049 Madrid, Spain

FEATURES
source Location/Qualifiers
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 /organism="Solanum tuberosum"
 /macronuclear
 /mol_type="mRNA"
 /sub_species="Desiree"
 /db_xref="taxon:4113"
 /haplotype="tetraploid"
 /cell_line="Desiree"
 /tissue_type="root"
 1..838
 /gene="pin2"
 /gene="pin2"
 /gene="pin2"
 /evidence=not_experimental

gene
sig_peptide
ORIGIN

Query Match 4.9%; Score 26; DB 8; Length 838;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 ATATGCCACGCTCAGAAGAGATCC 150
 |||||
Db 148 ATATGCCACGCTCAGAAGAGATCC 173

Search completed: August 22, 2005, 05:33:42
 Job time : 2495 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 00:20:26 ; Search time 421 Seconds
(without alignments)
7438.345 Million cell updates/sec

Title: US-10-725-829-1

Perfect score: 529

Sequence: 1 cataatggtcgttcacaaag.....ctgtaatgsgacttattcg 529

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	100.0	529	12 ADP02854	ADP02854 Solanum a
2	35	6.6	684	10 ADD05323	Add05323 Tin2 stru
3	27	5.1	584	3 AA249862	Aaz49862 Potato pr
4	26	4.9	1241	2 AAQ20253	Aaq20253 Wound-ind
5	21	4.0	56	12 ADP02865	ADP02865 Solanum a
6	20	3.8	471	8 ACA24243	Aca24243 Prokaryot
7	20	3.8	692	12 ADP02856	ADP02856 Solanum a
8	20	3.8	1104	2 AAO68728	Aag68728 Nucleotid
9	20	3.8	1104	6 ADI56863	Adi56863 Plant def
10	20	3.8	1360	2 AAO68729	Aag68729 Full leng
11	20	3.8	2375	4 ABL25042	Abi25042 Drosophila
12	20	3.8	8693	6 ABL32809	Abi32809 Human imm
13	19	3.6	360	13 ADR60668	Adr60668 Cotton cd
14	19	3.6	406	12 ADP92707	Adp92707 Cotton ex
15	19	3.6	875	13 ADR60667	Adr60667 Cotton cd
16	19	3.6	1988	4 AAD03720	Aad03720 Tomato ce
17	19	3.6	2180	8 ABV74326	Abv74326 Mouse MLZ
18	19	3.6	2180	13 ADR75242	Adr75242 Mouse gas
19	19	3.6	4066	4 AAH54963	Aah54963 S. epider
20	19	3.6	25899	12 ADQ59374	Adq59374 Human can

C	21	19	3.6	225587	12 ADQ97397	Adq97397 Human can
C	22	18	3.4	403	4 AAK72040	Aak72040 Human imm
C	23	18	3.4	717	8 ACA34508	Aca34508 Prokaryot
C	24	18	3.4	880	6 ABE65369	Abk65369 Arabidops
C	25	18	3.4	880	12 ADQ63054	Adq63054 Transcrip
C	26	18	3.4	1829	10 ADE58408	Ades8408 Human gen
C	27	18	3.4	2000	8 ADA72701	Ada72701 Rice gene
C	28	18	3.4	2056	10 ADR42471	Adr42471 Human pp9
C	29	18	3.4	2221	4 AAD11116	Aad11116 Human sma
C	30	18	3.4	2456	6 ABE61456	Abk61456 Human cdn
C	31	18	3.4	2581	12 ADQ86085	Adq86085 Human lum
C	32	18	3.4	12581	13 ACN38037	Acn38037 Tumour-as
C	33	18	3.4	2636	10 ADB62481	Adb62481 Human cdn
C	34	18	3.4	2803	10 ADB63758	Adb63758 Human cdn
C	35	18	3.4	2898	4 AAL06787	Aal06787 Human rep
C	36	18	3.4	2898	4 AAL06788	Aal06788 Human rep
C	37	18	3.4	2898	4 ABA08061	Abao8061 Human ova
C	38	18	3.4	2898	4 ABA08062	Abao8062 Human ova
C	39	18	3.4	2907	5 AAI58623	Aai58623 Human pol
C	40	18	3.4	2907	5 ADQ98841	Adq98841 DNA encod
C	41	18	3.4	2907	9 ADB48601	Adb48601 Novel hum
C	42	18	3.4	2968	4 AAI60409	Aai60409 Human pol
C	43	18	3.4	4356	8 ACA39352	Aca39352 Prokaryot
C	44	18	3.4	4908	8 ACA45174	Aca45174 Prokaryot
C	45	18	3.4	5875	6 ABL32288	Abi32288 Human imm

ALIGNMENTS

RESULT 1	ADP02854	standard; DNA; 529 BP.
ID	ADP02854	
AC	ADP02854;	
XX	XX	
DT	09-SEP-2004 (first entry)	
XX	XX	
DE	Solanum americanum proteinase inhibitor II gene Sapin2a.	
XX	XX	
KM	de; gene; proteinase inhibitor II; transformed plant; resistance; insect;	
KW	pest; pathogen; programmed cell death; senescence.	
XX	XX	
OS	Solanum americanum;	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	5..451
FT		/*tag= a
FT		/product= "Sapin2a protein"
XX	XX	
PN	WO2004050873-A1.	
XX	XX	
PD	17-JUN-2004.	
XX	XX	
PF	01-DEC-2003; 2003WO-CN001020.	
XX	XX	
PR	29-NOV-2002; 2002US-O429992P.	
XX	XX	
PA	(UYHK-) UNIV HONG KONG.	
XX	XX	
PI	Chye M, Xu Z, Sin S;	
XX	XX	
DR	WPI; 2004-450731/42.	
XX	XX	
DR	P-PSDB; ADP02855.	
XX	XX	
PT	New proteinase inhibitor, Sapin2a or Sapin2b, useful in producing	
PT	transformed plants having enhanced resistance to insects, pest or	
PT	pathogens and in which programmed cell death or senescence is inhibited.	
XX	XX	
PS	Claim 1, SEQ ID NO 1, 90pp; English.	
XX	XX	
CC	The invention relates to an isolated proteinase inhibitor II nucleic acid	
CC	molecule (1). The proteinase inhibitor II nucleic acid molecule and the	

31-JUL-2002.
xx
xx

XX
PN
XX
WO200004049-A1.

31-JUL-2002.
xx
xx

XX
PN
XX
WO200004049-A1.

```

PD 27-JAN-2000.
XX
XX 15-JUL-1999; 99WO-NZ000110.
XX
XX 15-JUL-1998; 98NZ-00331002.
XX
XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
XX
XX Christeller JT, Sutherland PW, Murray C, Markwick NP, Philip BA,
XX Malone LA, Burgess EPJ;
XX WPI; 2000-171244/15.
XX
XX New chimeric polypeptide and composition comprising the polypeptide
XX useful for conferring pest resistance on plants.
XX
XX Example 3; Fig 4; 11pp; English.
XX
XX The present sequence encodes potato proteinase inhibitor-II (PII-II).
XX This is used in the preparation of a binary vector designed to express a
XX chimeric polypeptide comprising streptavidin mature peptide, a plant-
XX noxious protein, fused to the PII-II signal peptide. The binary vector is
XX targeted to the vacuole by PII-II signal sequence. Transformation of
XX plant genome with the vector can produce pest resistance in plants, plant
XX derived products and stored harvest material. Pests that can be
XX controlled include, cotton bollworm, tropical army-worm, European corn -
XX borer or red mite, tobacco horn worm, loopers, rice stem borer, porina,
XX cutworms, diamondback moth, potato tuber moth, codling moth, Indian meal
XX moth, gypsy moth, Argentine stem weevil, clover root weevil, grass -
XX grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles,
XX black field cricket, locusts, sawflies, Western flower thrips, Hessian
XX flies or two-spotted mite
XX
XX Sequence 584 BP; 184 A; 94 C; 116 G; 190 T; 0 U; 0 Other;
SQ
Query Match 5.1%; Score 27; DB 3; Length 584;
Best Local Similarity 100.0%; Pred.No. 0.0026;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 CAATTGTTGCTCAGGCTATAAGGCTTG 195
DB 296 CAATTGTTGCTCAGGCTATAAGGCTTG 322
RESULT 4
ID AAQ20253 standard; DNA; 1241 BP.
XX
XX AAQ20253;
XX
XX 24-MAR-1992 (first entry)
XX
XX Wound-inducible potato protease inhibitor IIX gene.
XX
XX methyl jasmonate; transgenic plant; predator defence protein; ss.
XX
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX TATA_signal 227..231 /*tag= d
XX exon 306..357 /*tag= a
XX intron /*number= 1
XX intron 358..474 /*tag= b
XX exon 475..884 /*number= 1
XX intron /*tag= c
XX exon /*number= 2
XX polyA_signal 1019..1024 /*tag= e
XX

```

```

PN W09118512-A.
XX
XX 12-DEC-1991.
XX
XX 25-MAY-1990; 90US-00528956.
XX
XX 25-MAY-1990; 90US-00528956.
XX
XX (UNIW ) WASHINGTON STATE UN.
XX
XX Ryan CA, Farmer EE;
XX WPI; 1992-007120/01.
XX
XX P-PSDB; AAR20099.
XX
XX Induction of defence protein prodn. in plants - by treatment with agent
XX capable of such induction, esp. Jasmonic acid cpd.
XX
XX Example 7; Fig 6; 40pp; English.
XX
XX A Russett Burbank potato genomic library was screened by using nick-
XX translated wound-induced tomato inhibitor II cDNA as a probe. Positive
XX clones were rescreened and a clone contg. an 8bp EcoRI insert hybridised
XX most strongly with the probe. A TaqI 2.6kbp fragment of this insert was
XX subcloned in M13 and a 1.24kbp fragment sequenced. The nucleotide
XX sequence of the potato inhibitor IIX gene is similar to an inhibitor II
XX gene isolated from the diploid potato line HH80 12017 (see Keil, M et
XX al., Nucleic Acids Res. 14:5641-5650, 1986)
XX
XX Sequence 1241 BP; 430 A; 188 C; 223 G; 400 T; 0 U; 0 Other;
SQ
Query Match 4.9%; Score 26; DB 2; Length 1241;
Best Local Similarity 100.0%; Pred.No. 0.0085;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 ATATGCCACGTTCCAGAGGAAGTCC 150
DB 552 ATATGCCACGTTCCAGAGGAAGTCC 577
RESULT 5
ID ADP02865 standard; DNA; 56 BP.
XX
XX ADP02865;
XX
XX 09-SEP-2004 (first entry)
XX
XX Solanum americanum proteinase inhibitor II gene Sapin2a primer M1399.
XX
XX ss; primer; proteinase inhibitor II; transformed plant; resistance;
XX insect; pest; pathogen; programmed cell death; senescence.
XX
XX Solanum americanum.
XX
XX W02004050873-A1.
XX
XX 17-JUN-2004.
XX
XX 01-DEC-2003; 2003WO-CN001020.
XX
XX 29-NOV-2002; 2002US-0429992P.
XX
XX (UYHK-) UNIV HONG KONG.
XX
XX Chye M, Xu Z, Sin S;
XX WPI; 2004-450731/42.
XX
XX New proteinase inhibitor, Sapin2a or Sapin2b, useful in producing
XX transformed plants having enhanced resistance to insects, pest or
XX pathogens and in which programmed cell death or senescence is inhibited.
XX

```

PS Example; SEQ ID NO 12; 90pp; English.
 CC The invention relates to an isolated proteinase inhibitor II nucleic acid
 CC molecule (1). The proteinase inhibitor II nucleic acid molecule and the
 CC encoded polypeptide, methods are useful in producing transformed plants
 CC having enhanced resistance to insects, pest or pathogens and in which
 CC programmed cell death or senescence is inhibited. This sequence
 CC corresponds to a PCR primer to amplify the American black nightshade
 CC SAPIIN2a gene, used or screen for integration of the SAPIIN2a cDNA in
 CC plasmid-transformed tobacco plants.
 SQ Sequence 56 BP; 17 A; 15 C; 9 G; 15 T; 0 U; 0 Other;
 Query Match 4.0%; Score 21; DB 12; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 ATGGCTGTTCAACAAAGTTAGC 25
 DB 36 ATGGCTGTTCAACAAAGTTAGC 56
 RESULT 6
 ID ACA24243/c
 AC ACA24243;
 XX
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #5900.
 XX
 XX Antisense; ds; prokaryotic essential gene; cell proliferation;
 KM drug design; gene.
 XX
 OS Bacteroides fragilis.
 XX
 PN WO200277183-A2.
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00949593.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362659P.
 XX
 PA (ELITRA) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR MPI: 2003-029936/02.
 DR P-PSDB; AB020373.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 12113; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 471 BP; 162 A; 54 C; 93 G; 162 T; 0 U; 0 Other;
 Query Match 3.8%; Score 20; DB 8; Length 471;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 466 TTATCTATCAAAAAAAAAATA 485
 DB 176 TTATCTATCAAAAAAAAAATA 157
 RESULT 7
 ID ADP02856
 AC ADP02856;
 XX
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Solanum americanum proteinase inhibitor II gene SAPIIN2B.
 XX
 KM ds; gene; proteinase inhibitor II; transformed plant; resistance; insect;
 KM pest; pathogen; programmed cell death; senescence.
 XX
 OS Solanum americanum.
 XX
 PN Key Location/Qualifiers
 FT CDS 33..491
 FT /*tag= a
 FT /product= "SAPIIN2b protein"
 XX
 PD WO2004050873-A1.
 XX
 PF 17-JUN-2004.
 XX
 PR 01-DEC-2003; 2003WO-CN001020.
 PR 29-NOV-2002; 2002US-042992P.
 XX
 PA (UYHK-) UNIV HONG KONG.
 XX
 PI Chye M, Xu Z, Sin S;
 PI MPI: 2004-450731/42.
 DR P-PSDB; ADP02857.
 XX
 PT New proteinase inhibitor, SAPIIN2a or SAPIIN2b, useful in producing
 PT transformed plants having enhanced resistance to insects, pest or
 PT pathogens and in which programmed cell death or senescence is inhibited.
 XX
 PS Claim 2; SEQ ID NO 3; 90pp; English.

XX The invention relates to an isolated proteinase inhibitor II nucleic acid
 CC molecule (I). The proteinase inhibitor II nucleic acid molecule and the
 CC encoded polypeptide, methods are useful in producing transformed plants
 CC having enhanced resistance to insects, pest or pathogens and in which
 CC programmed cell death or senescence is inhibited. This sequence
 CC corresponds to the American black nightshade Sapindb gene.

XX Sequence 692 BP; 229 A; 113 C; 148 G; 202 T; 0 U; 0 Other;

Query Match 3.8%; Score 20; DB 12; Length 692;

Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;

Db 170 AATTGTTCTCAGCTATTA 189
 |||||
 210 AATTGTTCTCAGCTATTA 229

RESULT 8

AA068728 ID AA068728 standard; DNA; 1104 BP.

XX AA068728;

XX 25-MAR-2003 (revised)

DT 02-MAR-1995 (first entry)

XX Nucleotide coding region of N-alata PI precursor.

XX Type II serine proteinase inhibitor precursor; PI; tobacco;
 KW transgenic plant; anti-pathogen; anti-predator; ss.

XX Nicotiana alata.

XX Key Location/Qualifiers

FT CDS 1..1104

XX W09413810-A1.

XX 23-JUN-1994.

XX 16-DEC-1993; 93WO-AU000659.

XX 16-DEC-1992; 92AU-00006399.

XX (UYME) UNIV MELBOURNE.

XX Anderson MA, Atkinson AH, Heath RL, Clarke AE;

XX WPI; 1994-217886/26.

XX P-PSDB; AAR54135.

XX Nicotiana alata type II serine protease inhibitor precursor and DNA -

XX useful in ppxdn of anti-pathogen or anti-predator constructs for plants.

XX Claim 5; Page 44-45; 83pp; English.

XX A cDNA library, prepd. from mRNA from the stigmas and styles of mature
 CC flowers of N. alata was screened for clones of highly expressed genes
 CC which were not associated with self-incompatibility genotype. Clones
 CC encoding a protein with some identity to the type II proteinase
 CC inhibitors from potato and tomato were selected. The largest clone, NA-PI
 CC -2, is given in AA068729. The predicted AA sequence in AAR54135. AA068728
 CC is the coding region of AA068729. A nucleic acid isolate having at least
 CC 5% similarity to AA068728 is claimed. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 1104 BP; 337 A; 176 C; 295 G; 296 T; 0 U; 0 Other;

Query Match 3.8%; Score 20; DB 2; Length 1104;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 AATTGTGAAGAGATCTGA 243
 |||||
 Db 1012 AATTGTGAAGAGATCTGA 1031

RESULT 9

AD156863 ID AD156863 standard; DNA; 1104 BP.

XX AD156863;

XX 22-APR-2004 (first entry)

XX Plant defensin Napi mature domain cDNA.

XX ds; gene; insecticide; antifungal; virucide; antibacterial;

XX flower development; plant pest resistance; floral defensin precursor;

XX transgenic plant; insect resistance.

XX Unidentified.

XX W0200263011-A1.

XX 15-AUG-2002.

XX 08-FEB-2002; 2002WO-AU000123.

XX 08-FEB-2001; 2001US-0267271P.

XX (HEXI-) HEXIMA LTD.

XX Anderson MA, Lay FT, Heath RL;

XX WPI; 2002-657538/70.

XX P-PSDB; AD156864.

XX New isolated plant floral defensin-like polypeptides and polynucleotides,

XX for generating transgenic plants having resistance or at least reduced

XX sensitivity to plant pests including insects, microorganisms, fungi

XX and/or viruses.

XX Disclosure; SEQ ID NO 56; 164pp; English.

XX The invention relates to an isolated polypeptide comprising, in its
 CC precursor form, an N-terminal signal domain, a mature domain and an
 CC acidic C-terminal domain, where the polypeptide is produced during flower
 CC development and its mature domain has activity against one or more plant
 CC pests. Plant floral defensin-like polypeptides and polynucleotides are
 CC useful in generating transgenic plants having resistance or at least
 CC reduced sensitivity to plant pests including insects, microorganisms,
 CC fungi and/or viruses. They are also useful in generating recombinant
 CC defensin-like molecules for use in the topical application of
 CC compositions to prevent or retard pest-infestation of plants. The floral-
 CC and seed-derived defensins are useful in the generation of insect
 CC resistance in plants. This sequence represents the cDNA encoding the
 CC mature domain from a plant defensin protein.

XX Sequence 1104 BP; 337 A; 176 C; 295 G; 296 T; 0 U; 0 Other;

Query Match 3.8%; Score 20; DB 6; Length 1104;

Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;

Qy 224 AATTGTGAAGAGATCTGA 243
 |||||
 Db 1012 AATTGTGAAGAGATCTGA 1031

RESULT 10

AA068729 ID AA068729 standard; DNA; 1360 BP.

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XX AC AA068729;
XX DT 25-MAR-2003 (revised)
XX DT 02-MAR-1995 (first entry)
XX DE Full length sequence of PI precursor.
XX KW Type II serine proteinase inhibitor precursor; PI; tobacco;
XX KW transgenic plant; anti-pathogen; anti-predator; ss.
XX OS Nicotiana glauca.
XX FH Key Location/Qualifiers
XX FT msc_signal 1..97
XX FT /*tag= b
XX FT /label= signal sequence
XX FT 97..1200
XX FT /*tag= a
XX PN WO9413810-A1.
XX PD 23-JUN-1994.
XX PF 16-DEC-1993; 93WO-AU000659.
XX PR 16-DEC-1992; 92AU-00006399.
XX PA (UYME ) UNIV MELBOURNE.
XX PI Anderson MA, Atkinson AH, Heath RU, Clarke AE;
XX DR WPI, 1994-217886/26.
XX DR P-PSDB; AAR54135.
XX PT Nicotiana glauca type II serine proteinase inhibitor precursor and DNA -
XX PT useful in prodn of anti-pathogen or anti-predator constructs for plants.
XX PS Disclosure; Page 45-47; 83pp; English.
XX CC A cDNA library, prep'd. from mRNA from the stigmas and styles of mature
XX CC flowers of N. glauca was screened for clones of highly expressed genes
XX CC which were not associated with self-incompatibility genotype. Clones
XX CC encoding a protein with some identity to the type II proteinase
XX CC inhibitors from potato and tomato were selected. The largest clone, NA-PI
XX CC -2, is given in AA068729. The predicted AA sequence in AAR54135. (Updated
XX CC on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1360 BP; 416 A; 219 C; 345 G; 380 T; 0 U; 0 Other;
XX
XX Query Match 3.8%; Score 20; DB 2; Length 1360;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 224 ATTGTGAGAGAGATCTGA 243
XX DB 1108 ATTGTGAGAGAGATCTGA 1127
XX
XX RESULT 11
XX ID ABL25042/c
XX ID ABL25042 standard; DNA; 2375 BP.
XX AC ABL25042;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 26599.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX KW Drosophila melanogaster.
XX OS

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XX PN WO200171042-A2.
XX DT 27-SEP-2001.
XX DE 23-MAR-2001; 2001WO-US009231.
XX PF 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PMD, Myers EW;
XX DR WPI, 2001-656860/75.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Claim 1; SEQ ID NO 26599; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
XX CC AB572072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 2375 BP; 659 A; 530 C; 532 G; 654 T; 0 U; 0 Other;
XX
XX Query Match 3.8%; Score 20; DB 4; Length 2375;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 90 CTTGTACTGAGAGATGTGCT 109
XX DB 2024 CTTGTACTGAGAGATGTGCT 2005
XX
XX RESULT 12
XX ID ABL32809/c
XX ID ABL32809 standard; DNA; 8693 BP.
XX AC ABL32809;
XX DT 26-MAR-2002 (first entry)
XX DE Human immune system associated gene SEQ ID NO: 782.
XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
XX KW antiarteriosclerotic; antiangioma; cytostatic; noctropic;
XX KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX KW antineoplastic; antidiabetic; antidiabetic; antiparasitic;
XX KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
XX KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
XX KW ds.
XX OS Homo sapiens.
XX DT WO200200928-A2.
XX DE 03-JAN-2002.
XX PF 02-JUL-2001; 2001WO-BP007537.
XX PR 30-JUN-2000; 2000DE-01032529.
XX PR 01-SEP-2000; 2000DE-01043826.

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XX (EPiG-) EPIGENOMICS AG.
 XX PA
 XX PI Olek A, Piépenbrock C, Berlin K;
 XX DR WPI; 2002-130909/17.
 XX PT Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX PS
 XX Claim 1; SEQ ID NO 782; 32pp + Sequence Listing; German.
 XX CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 CC XX
 SQ Sequence 8693 BP; 2165 A; 182 C; 2239 G; 4107 T; 0 U; 0 Other;
 Query Match 3.8%; Score 20; DB 6; Length 8693;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 467 TATCTATCAAAAAAATAT 486
 DB 4122 TATCTATCAAAAAAATAT 4103
 RESULT 13
 ADR60668/c
 ID ADR60668 standard; cDNA; 360 BP.
 XX AC
 AC ADR60668;
 XX DT 02-DEC-2004 (first entry)
 XX DE Cotton cDNA sequence, SEQ ID 1449.
 XX CC Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
 KW drought tolerance; plant disease resistance; galactomannan; lignin;
 KW plant growth regulator; heat tolerance; herbicide tolerance;
 KW homologous recombination; extreme osmotic condition tolerance;
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 stress resistance.
 XX OS
 OS Gossypium hirsutum.
 XX PN US2004181830-A1.
 XX PD 16-SEP-2004.
 XX PF 29-JAN-2004; 2004US-00767795.
 XX PR 07-MAY-2001; 2001US-00849529.
 XX PR 12-DEC-2001; 2001US-00021323.
 XX PA (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAO/) CAO Y.
 XX PI Kovalic DK, Zhou Y, Cao Y;
 XX DR WPI; 2004-667718/65.
 PT New recombinant nucleic acid molecules and polypeptides from Gossypium
 PT hirsutum, useful for producing plants with improved biological
 PT characteristics (e.g. improved plant cold or drought tolerance).
 XX

PS Claim 1; SEQ ID NO 1449; 14pp; English.
 XX CC The invention relates to a recombinant polynucleotide comprising any of
 CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
 CC Also a recombinant polypeptide comprising any of the 58798 amino acid
 CC sequences mentioned in the specification and producing a plant having an
 CC improved property. Producing a plant having an improved property
 CC comprises transforming a plant with a recombinant construct comprising a
 CC promoter region functional in a plant cell operably joined to a
 CC polynucleotide comprising a coding sequence for a polypeptide associated
 CC with the property, and growing the transformed plant. The polypeptide is
 CC useful for improving plant cold tolerance, manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, improving plant
 CC drought tolerance, providing increased resistance to plant disease,
 CC producing galactomannan (or lignin or plant growth regulators), improving
 CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 CC the rate of homologous recombination in plants, improving plant tolerance
 CC to extreme osmotic conditions or to pathogens or pests, improving yield
 CC by modification of photosynthesis, modifying seed oil or protein yield
 CC and/or content, improving yield by modification of carbohydrate, nitrogen
 CC or phosphorus use and/or uptake, or improving yield by providing improved
 CC plant growth and development under at least one stress condition. The
 CC polynucleotide and polypeptide may also be used in recombinant DNA
 CC constructs, in physical arrays of molecules, as plant breeding markers,
 CC or in computer-based storage and analysis systems. The present sequence
 CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20040181830. However only 6585
 CC polynucleotide sequences were available, the remaining 52213
 CC polynucleotides and all 58798 protein sequences were not present.
 CC XX
 SQ Sequence 360 BP; 92 A; 68 C; 92 G; 108 T; 0 U; 0 Other;
 Query Match 3.6%; Score 19; DB 13; Length 360;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 272 GAATGTATACACAGATTG 290
 DB 170 GAATGTATACACAGATTG 152
 RESULT 14
 ADP92707/c
 ID ADP92707 standard; cDNA; 406 BP.
 XX AC
 AC ADP92707;
 XX DT 09-SEP-2004 (first entry)
 XX DE Cotton expressed sequence tag, EST, #1718.
 XX KW Cotton; ss; EST; expressed sequence tag; plant; plant protection;
 KW plant improvement; marker-assisted breeding.
 XX OS
 OS Gossypium hirsutum; variety NuCotton33B.
 XX PN US2004123338-A1.
 XX PD 24-JUN-2004.
 XX PF 08-DEC-2000; 2000US-00732627.
 XX PR 10-DEC-1999; 99US-0170255P.
 XX PA (FINC/) FINCHER K L.
 XX PI Fincher KL;
 XX DR WPI; 2004-479807/45.
 PT New substantially purified nucleic acid molecule that encodes a cotton

PT protein or its fragment, useful as molecular tool for the targeting and
 PT isolation of novel genes for plant protection and improvement.
 PS Claim 1, SEQ ID NO 1718; 30pp; English.
 CC The invention relates to a substantially purified nucleic acid molecule
 CC that encodes a cotton protein or its fragment comprising an EST
 CC (expressed sequence tag) appearing as ADP90990-ADP95919. Also included
 CC are a substantially purified cotton protein or its fragment encoded by a
 CC nucleic acid molecule comprising an exogenous promoter region which
 CC acid molecule which comprises: an exogenous promoter region which
 CC functions in a plant cell to cause the production of an RNA molecule; a
 CC structural nucleic acid molecule comprising one of the ESTs or their
 CC complements; a 3' non-translated sequence that functions in the plant
 CC cell to cause termination of transcription and addition of polyadenylated
 CC ribonucleotides to a 3' end of the mRNA molecule). The ESTs are useful as
 CC molecular tool for the targeting and isolation of novel genes for plant
 CC protection and improvement. The ESTs are useful for developing new
 CC strategies for understanding critical plant developmental and metabolic
 CC pathways, for isolating genes and promoters, for identifying and mapping
 CC the genes involved in developmental and metabolic pathways, and for
 CC determining gene function. The cotton nucleic acid molecules are useful
 CC as molecular tags to isolate genetic regions, isolate genes, map genes,
 CC and determine gene function. The nucleic acid molecules are useful for
 CC determining if genes are members of a particular gene family and for use
 CC in marker-assisted breeding programs. The present sequence is one of the
 CC 4930 cotton ESTs of the invention. NOTE: The sequences are not displayed
 CC in the specification but are available in electronic format from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docid=20040123338.
 CC XX
 SO Sequence 406 BP; 105 A; 95 C; 92 G; 114 T; 0 U; 0 Other;
 Query Match 3.6%; Score 19; DB 13; Length 406;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 272 GAATGTGATACACAGATTG 290
 DB 398 GAATGTGATACACAGATTG 380
 RESULT 15
 ADR60647/C
 ID ADR60647 standard; cDNA; 875 BP.
 XX
 AC ADR60647;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Cotton cDNA sequence, SEQ ID 1428.
 XX
 KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
 KW drought tolerance; plant disease resistance; galactomannan; lignin;
 KW plant growth regulator; heat tolerance; herbicide tolerance;
 KW homologous recombination; extreme osmotic condition tolerance;
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 KW stress resistance.
 XX
 OS Gossypium hirsutum.
 XX
 PN US2004181830-A1.
 XX
 PD 16-SEP-2004.
 XX
 PF 29-JAN-2004; 2004US-00767795.
 XX
 PR 07-MAY-2001; 2001US-00849529.
 XX
 PR 12-DEC-2001; 2001US-00021323.
 XX
 PA (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAOY/) CAO Y.
 XX

PI KOVALIC DK, Zhou Y, Cao Y;
 XX MPI, 2004-667718/65.
 XX
 PT New recombinant nucleic acid molecules and polypeptides from Gossypium
 PT hirsutum, useful for producing plants with improved biological
 PT characteristics (e.g. improved plant cold or drought tolerance).
 XX
 PS Claim 1, SEQ ID NO 1428; 14pp; English.
 XX
 CC The invention relates to a recombinant polynucleotide comprising any of
 CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
 CC Also a recombinant polypeptide comprising any of the 58798 amino acid
 CC sequences mentioned in the specification and producing a plant having an
 CC improved property. Producing a plant having an improved property
 CC comprises transforming a plant with a recombinant construct comprising a
 CC promoter region functional in a plant cell operably joined to a
 CC polynucleotide comprising a coding sequence for a polypeptide associated
 CC with the property, and growing the transformed plant. The polypeptide is
 CC useful for improving plant cold tolerance, manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, improving plant
 CC drought tolerance, providing increased resistance to plant disease,
 CC producing galactomannan (or lignin or plant growth regulators), improving
 CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 CC the rate of homologous recombination in plants, improving plant tolerance
 CC to extreme osmotic conditions or to pathogens or pests, improving yield
 CC by modification of photosynthesis, modifying seed oil or protein yield
 CC and/or content, improving yield by modification of carbohydrate, nitrogen
 CC or phosphorus use and/or uptake, or improving yield by providing improved
 CC plant growth and development under at least one stress condition. The
 CC polynucleotide and polypeptide may also be used in recombinant DNA
 CC constructs, in physical arrays of molecules, as plant breeding markers,
 CC or in computer-based storage and analysis systems. The present sequence
 CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20040181830. However only 6585
 CC polynucleotide sequences were available, the remaining 52213
 CC polynucleotides and all 58798 protein sequences were not present.
 CC XX
 SQ Sequence 875 BP; 271 A; 170 C; 194 G; 240 T; 0 U; 0 Other;
 Query Match 3.6%; Score 19; DB 13; Length 875;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 272 GAATGTGATACACAGATTG 290
 DB 431 GAATGTGATACACAGATTG 413
 Search completed: August 22, 2005, 03:57:17
 Job time : 427 secs